International Journal on Recent and Innovation Trends in Computing and Communication
ISSN: 2321-8169 Volume: 11 Issue: 5s
DOI: https://doi.org/10.17762/ijritcc.v11i5s.6647
***Article Received**: 28 February 2023 **Revised**: 04 April 2023 **Accepted**: 20 April 2023*

Malarial Diagnosis with Deep Learning and Image Processing Approaches

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Abstract— Malaria is a mosquito-borne disease that has killed an estimated a half-a-million people worldwide since 2000. It may be time consuming and costly to conduct thorough laboratory testing for malaria, and it also requires the skills of trained laboratory personnel. Additionally, human analysis might make mistakes. Integrating denoising and image segmentation techniques with Generative Adversarial Network (GAN) as a data augmentation technique can enhance the performance of diagnosis. Various deep learning models, such as CNN, ResNet50, and VGG19, for recognising the Plasmodium parasite in thick blood smear images have been used. The experimental results indicate that the VGG19 model performed best by achieving 98.46% compared to other approaches. This study demonstrates the potential of artificial intelligence to improve the speed and precision of pathogen detection which is more effective than manual analysis.

Keywords- Deep learning, CNN, ResNet50, VGG19, noise reduction, image segmentation, GAN, optimization methods.

I. INTRODUCTION

Malaria is a serious global health concern, particularly in tropical and subtropical regions. Diagnostic procedures for malaria, which require experienced laboratory personnel and microscopy, can be both time-consuming and expensive [1]. Delays in diagnosis and treatment can worsen the patient's condition and even lead to fatalities. The Plasmodium parasite, responsible for causing malaria, has a complex life cycle involving human hosts and female Anopheles mosquitoes. Female mosquitoes infected with the parasite can transmit it to humans by injecting sporozoites into the bloodstream circulation during a bite which can be seen in Figure1.

The parasite then infects liver cells and reproduces asexually, releasing dozens of merozoites that invade red blood cells and multiply again [3]. The cycle continues, leading to the destruction of red blood cells and symptoms of malaria. Gametocytes, the male and female forms of the parasite, can be picked up by another mosquito during a blood meal, leading to the formation of an ookinete that must break through the mosquito's midgut wall to mature into an oocyst. The oocyst releases sporozoites into the mosquito's hemocoel and eventually into the mosquito's salivary glands, where it can be transmitted to a new human host during a blood meal. Understanding the intricate life cycle of the Plasmodium parasite and its interactions with human and mosquito hosts is crucial for effective prevention and treatment of malaria.

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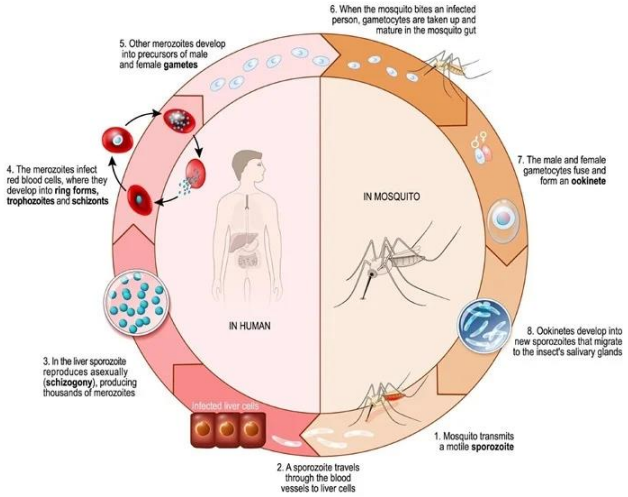

Figure 1: Life Cycle of Plasmodium Parasite [25].

In 2019, the World Health Organization predicted that malaria would afflict 229 million people worldwide, with most cases and deaths occurring in sub-Saharan Africa. Pregnant women and young children are particularly susceptible to the disease. The COVID-19 pandemic has exacerbated concerns about malaria, as many countries have struggled to maintain prevention and treatment systems. Despite these challenges, progress has been made in recent years, with reductions in malaria incidence and deaths reported in several countries. The World Health Organization's Global Technical Plan for Malaria, 2016-2030, sets ambitious targets, including a 90% decrease in malaria incidence and mortality by 2030. Achieving these targets will require sustained efforts to develop new prevention and treatment strategies, as well as continued investment in existing tools and resources.

Malaria is a major public health concern affecting millions of people worldwide, and traditional diagnostic methods are often slow and labor-intensive. However, recent advancements in deep learning have shown great promise in improving the accuracy and efficiency of malaria detection. By training on large datasets of labeled images, deep learning algorithms can identify subtle patterns and features in blood smears that may not be visible to the human eye. In this study, deep learning approaches such as Convolutional Neural Networks (CNNs), Residual Network 50 (ResNet50), and Visual Geometry Group 19 (VGG19) have been implemented to detect the Plasmodium parasite in thick blood smear images. To improve the models' performance, noise reduction and image segmentation techniques, along with Generative Adversarial Networks (GANs) as a data augmentation strategy, have been employed. These techniques have the potential to significantly improve malaria detection, leading to earlier diagnosis and treatment, and ultimately, better outcomes for patients.

II. Literature Review

Wherever Times is specified, Times Roman or Times New Roman may be used. If neither is available on your word processor, please use the font closest in appearance to Times. Avoid using bit-mapped fonts if possible. True-Type 1 or Open Type fonts are preferred. Please embed symbol fonts, as well, for math, etc.

This section presents comprehensive literature on the recent deep learning architectures, noise removal, image segmentation, and data augmentation implemented to the thick blood smear images dataset.

Zhaohui Liang et al. (2021) introduced an innovative technique to generate patterns in blood cell images that are relevant for malaria using the Ad Cycle GAN model. This model incorporates a random element into an otherwise uniform image template, and it is made up of a convolutional variational autoencoder (CVAE) and a traditional cycle-consistent Generative adversarial network (Cycle GAN). After 150 iterations of optimization, a pretrained classifier is used to compare the synthetic images to real-world malaria cases. This architecture provided better classification than pre-existing methods [1].

Aimon Rahman et al. (2019) used end-to-end deep learning methods to enhance malaria classification using segmented red blood cell smear images. Authors evaluated the effects of many pre-processing procedures, including standardization, normalizing, and stain normalization, and concluded that none improved the model's performance. Instead, using data augmentation techniques on the training set yielded encouraging results. Moreover, the authors tried out several network topologies, such as a custom network architecture, fine-tuning on pre-trained models, and feature extraction using a convolutional neural network (CNN) trailed by a support vector machine classifier (SVM). Authors picked the TL-VGG16 (Transfer Learning-Visual Geometry Group) model because it had the highest accuracy of any of the suggested models, at 97.77 percent on the testing phase [2].

Six different architectures of convolutional neural network were used by Krit Sriporn et al. (2020) to verify and analyze a dataset of 7,000 images: Xception, Inception-V3, ResNet-50, NasNetMobile, VGG-16, and AlexNet. By evaluating 10% of non-dataset training and testing images using this model, the authors achieved an accuracy level of 98.86% utilizing Xception and the state-of-the-art activation function (Mish) and optimizer (adam). The authors emphasize the important factors that might assist in developing a better computer-aided diagnostic system for malaria diagnosis. When taken as a whole, the findings highlight the promise of convolutional neural networks for reliable malaria diagnosis [3].

Using Faster regions with convolutional neural networks (RCNN) in association with Feature Pyramid Network (FPN)

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and ResNet50, Hanung Adi Nugroho et al. (2021) developed a deep learning-based solution to malaria parasite detection. The proposed method was developed to reduce the number of false positive malaria parasite detections that had previously occurred using more conventional methods. The findings show that, in comparison to the conventional method, the suggested strategy greatly decreased both false positives and computing time. According to this author's study, parasites in thick blood smear images at the microscopic level may be automatically localized with high performance and faster than traditional methods [4].

Fast convolutional neural networks (CNNs) were suggested for the categorization of cell images by Barath Narayanan et al. (2019). The authors looked at using CAD (Computer-Aided Diagnosis) for diagnosing Plasmodium parasite on thick blood-smeared images, and they found that architectures like AlexNet, ResNet, VGG-16, and DenseNet were effective. CAD systems are a kind of computer system that may be used as a second opinion in the detection and/or diagnosis of medical conditions. One of the primary goals of these CAD systems is to speed up the process of image interpretation while simultaneously increasing radiologists' precision. To prevent the viewer from seeing a change in color while viewing an image in changing lighting, all images are down sampled to 50x50 pixels before being pre-processed using a color constancy algorithm. The author then used a 3x3 convolution operation, normalization, the rectified linear unit (ReLU), and a maxpooling layer with a 2x2 window and a stride of 2 to label images of cells. To further adjust and stabilize the model's performance, the author used the gradient descent with momentum optimization algorithm with an initial learning rate of 0.0001 and a modest batch size of 64. Finally, authors compared the utilized classification approaches (as mentioned earlier) using some evaluation metrics like accuracy, AUC curve and ultimately decided to take the VGG-16 model because of it having 96.5% accuracy than the other models for the malaria parasite dataset [5].

A convolutional neural network (CNN) model was recommended by Angel Molina et al. (2021) for automatically identifying RBCs infected with malaria parasites, as it can differentiate parasitized RBCs from both regular RBCs and RBCs comprising other types of inclusions that are scattered across the RBC's surface. As these RBC inclusions are all slightly irregular in shape, they may be easily distinguished from one another using standard image processing techniques such as edge detection and watershed transformation. Many unique CNN architectures were utilized to bring this model to life which are AlexNet, ResNet, SqueezeNet, DenseNet, VGG, Xception, and Inception. VGG has been used for technical reasons just because it is a transfer learning model, which produces better results with fewer layers of complexity. It allows the clinical pathologist to make a rapid, objective, and accurate morphological assessment, which speeds up the turnaround time [6].

Shruti Sinha et al. (2021) evaluated the ResNet (Residual Network) model with sequential models using stochastic gradient descent (SGD) as an optimizer and binary cross entropy as a loss function, and determine how accuracy relates to the model's layer depth. The dataset used and/or retrieved is composed of 27,558 images of cells and was collected from the US National Library of Medicine where Infected and uninfected individuals each make up of half of the data set. The ResNet model, with its many hidden layers, has been demonstrated to be superior to the sequential model in the detection of malaria in cell images. In conclusion, the author asserts that adding additional layers does not significantly enhance accuracy [7].

To automatically distinguish between parasitized and unparasitized cellular components in microscopic blood smear images, Priyadarshini Adyasha Pattanaik et al. (2021) create a state-of-the-art general-purpose deep-learning model of the depth filter bridge. They classify the data by using the combination of the Fisher vector (FV) with cross-stacked denoising autoencoder (SAE). Using an Extreme Learning Machine (ELM) as the ensemble's final base classifier, the author was able to significantly increase the system's learning speed. Together with SAE's encoder, a decoder was used to form a deep neural network. Via unsupervised learning, an encoder will ultimately seek to produce an output that is identical to the input. With the use of conceptual statistical models and discriminative models, the FV pooling operation unifies previously isolated data points. These mentioned layers are then combined to classify the malaria data. Not only does this model make the image more robust against noise, but it also makes it more robust against other sorts of variations. Finally, the author's findings show that this model outperformed the competing models including CNN, deep belief network (DBN), and AlexNet [8].

By utilizing a deep transfer graph convolutional network (DTGCN), Sen Li et al. (2021) developed a deep learning model for malaria parasite identification. Parts of the proposed DTGCN architecture include the unsupervised graph convolutional network (UGCN), source transfer graph development, and CNN feature extraction. First, images of all types are fed into a convolutional neural network (CNN), which is trained to identify and extract morphological features. Having established the need for class correlations between the different source class groups and the samples that would serve as targets, the author next outlined a method for building a source transfer graph. In the last step of the model, the author used a Graph Convolutional Network (GCN) to generate visuals of each feature set and group the source classes without human supervision. Finally, authors suggested that the K-means clustering technique was important

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in developing the appropriate network feature for classifying malaria parasites over a spectrum of life cycles [9].

Object recognition and segmentation using the Mask R-CNN method have been effectively implemented in several clinical settings. Important for both the diagnosis and treatment of malaria, this method was used by De Rong Loh et al. (2020) to detect infected red blood cells. Researchers also applied the watershed segmentation technique, which allows for a more rapid and accurate imaging of infected cells than previous models. The model is useful since it can count cells quickly and automatically, which is important in the medical field. The Region Proposal Network (RPN) and other transfer learning techniques were used to retrieve the ROIs and scores from the extracted feature maps. These methods make the model flexible enough to learn and adapt to new tasks with less input, which improves its use for medical diagnosis and treatment. Using the confusion matrix and the mean average accuracy, the authors analyzed the model's efficiency. These parameters were used to assess the model's ability to detect malaria-infected red blood cells, and the results show that the author's proposed model has great potential as a healthcare tool for malaria diagnosis than the other previously proposed models [10].

To address the problem of insufficient labelled data, Kitsuchart Pasupa et al. (2020) trained a semi-supervised deep convolutional generative adversarial network (DCGAN) to classify RBCs according to their morphology. As compared to the traditional CNN, the author's proposed model DCGAN performs better when fewer labels are used. Comparatively, CNN needs more labelled data to match the performance of DCGAN. DCGAN is made up of two neural networks: the discriminator and the generator. To prevent the discriminator from being fooled by a fake sample, the generator generates a fresh sample from the latent space that is as realistic as possible. Using a semi-supervised DCGAN strategy, author's shows that how well RBCs can be classified according to their morphology. This method can compensate for the lack of labelled data and get better results than the standard CNN, even with fewer examples. Finally, authors suggested that this study sheds light on the promising future of employing GANs for medical image analysis [11], which is an active field of research.

III. METHODOLOGY

This section provides a detailed explanation of how the research was conducted, from the collection and pre-processing of the data to the analysis and interpretation of the results on malaria identification using deep learning. It would demonstrate the validity and reliability of the findings and help readers to replicate the study in future research.

In this study, a total of 4000 images (2000 - infected and 2000 - uninfected) were collected from the internet, and a dataset description is provided in the following sections. The training, validation, and testing phases were then carried out, with 2800 samples in the training set and 1200 in the testing set.

To segment the thick blood smear pictures, noise reduction techniques and image segmentation methods were combined due to the shared same RGB intensity range of healthy and infected cells. The median blur with Otsu's thresholding (MBOT) was found to be the best method, and a data augmentation technique using a Cycle GAN was employed to increase the model's performance by adding more random image data series. Keras' flow from dataframe function was used to import and resize the training and testing images. The Adam optimization approach was used in three deep learning models, namely CNN, ResNet50, and VGG19, which are briefly described in the following sections. Evaluation criteria such as accuracy, loss, and time functions were used to compare the models, and the most suitable option was selected. The proposed technique is depicted as a flowchart in Figure 2, which can be seen below.

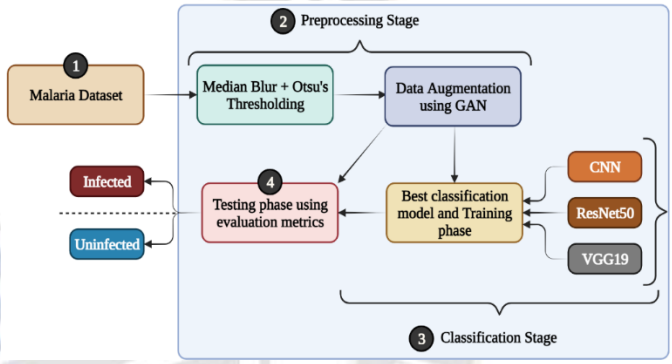

Figure 2: Flowchart of the steps involved in proposed methodology.

A. Malaria Dataset:

The data used in our research was sourced from Kaggle, a well-known online platform for competitions and data science projects. The dataset utilized comprises two primary directories: "Infected" and "Uninfected" which can be downloaded from the link (https://www.kaggle.com/datasets/iarunava/cell-images-for-detecting-malaria). The "Infected" directory contains images of thick blood smear red blood cells (RBCs) that have been infected with malaria parasites, while the "Uninfected" directory contains images of healthy thick blood smear RBCs. This dataset is a valuable resource for researchers studying malaria diagnosis using deep learning techniques, as it provides a diverse range of high-quality images that can be used to train and test deep learning models. To ensure the accuracy and reliability of our results, we carefully curated the dataset, eliminating any images that did not meet our rigorous quality standards.

B. Data Pre-processing Stage:

After conducting several studies on noise reduction and image segmentation, it is observed that combining median blur and Otsu's thresholding produced the best results for the malaria cell image dataset. When applied to a specific image dataset,

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such as one consisting of malaria cell images, the median blur Otsu's thresholding (MBOT) technique effectively removes noise and segments the images. Combining these two methods results in clean and well-defined images by reducing noise in the malaria cell images and separating the cells from the background, which will enhance the accuracy of the model.

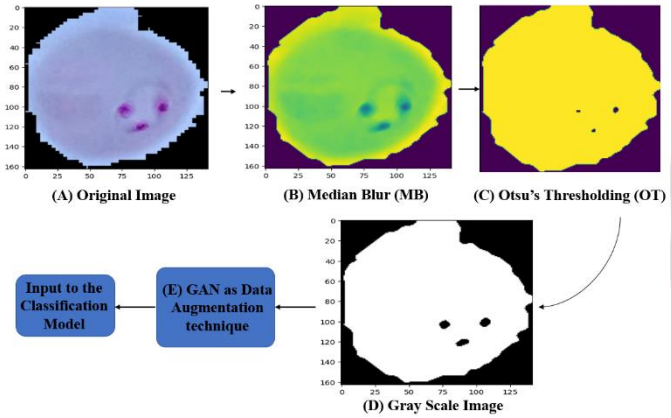

Figure 3: Pre-processing steps on a sample infected thick blood smear image.

1) Original Image:

In the context of malaria diagnosis using deep learning, the original image refers to the digital image that is directly obtained from the online source, which in this case is the Kaggle dataset. These images depict either infected or uninfected thick blood smear red blood cells (RBCs), which are the key elements in malaria diagnosis.

From figure 3 it is observed that the infected cell images contain certain distinguishing features, such as the presence of pores that are created when the Plasmodium parasite bursts out of the RBC. These pores can be observed on the edges of the infected RBC, and they serve as important markers for identifying infected cells. On the other hand, the uninfected cell images do not have any such pores on their cell edges and appear as a clean and healthy layer on the surface of the RBC, which is indicative of the absence of the Plasmodium parasite.

To improve the efficiency and accuracy of the deep learning model, the original images undergo several pre-processing steps, including image enhancement and augmentation techniques. Overall, by refining and synthesizing these original images, we build more effective models that are capable of accurately and efficiently identifying infected RBCs and contributing to the fight against this deadly disease.

2) Noise Removal using Median Blur (MB):

The median blur method of noise reduction in image processing adjusts the value of a single pixel to match the average of its surrounding neighbors. Salt-and-pepper noise, a kind of impulsive noise in which individual pixels have abnormally high or low values relative to their neighbors, may be pretty much eliminated using this technique. Since the median value represents the midpoint of a group of data, it is less impacted by extreme values and more effective in eliminating noise without distorting the central tendency. Sliding a window of a certain size across the picture and calculating the median of the pixel values inside the window at each place is how the median blur method works. The median value is then used to swap out the central pixel value with the new one. Imagine a M x N pixel picture with a window of size M x N that is centered at (x, y). Here's how to figure out the median:

Initialize an empty array of window pixel values as the first step. The second step is to compile a list of all the pixel values (i, j) that fall inside the window. Finally, put the pixel values in a sorted array. Fourth, if the window's number of pixels is odd, the middle value should be returned as the median. Finally, if the window's pixel count is divisible by 2, i.e., even, take the mean of the middle two values and report it as the median. This method is repeated for each pixel in the picture, with the computed median value replacing the pixel intensity at (x, y). Median blur noise reduction typically employs a square window of size 3 x 3, although other shapes (such as rectangles and circles) and sizes are possible. We can see from Figure 3 that the median blur noise reduction method is utilized on the infected cell image.is utilized on infected cell image.

3) Image segmentation using Otsu's Thresholding (OT):

Otsu's segmentation is an image segmentation method that determines the optimal threshold value for distinguishing between object and background pixels. The significance of Otsu's segmentation lies in its ability to automate the process of threshold selection. Prior to its development, threshold selection was often done manually, which was time-consuming and subjective. Otsu's segmentation method calculates the optimal threshold value by maximizing the between-class variance of the grayscale image, thereby providing an objective and automated threshold selection process. This technique may be used for a variety of purposes in the field of image processing, notably in the areas of computer vision and pattern recognition. Object detection, edge tracking, and image segmentation are just few of the applications that have made use of it. Otsu's segmentation is especially helpful in situations in which the images exhibit bimodal intensity distributions. This is usually the scenario in medical imaging and remote sensing applications, two fields that make frequent use of the technology. In general, Otsu's segmentation is an essential tool in image processing. It has made the procedure of threshold selection more efficient and objective, which can make it a good fit for the thick blood smear pictures dataset. This approach works well with images that have objects that are clearly defined, basic structures, and low noise levels. Because the malaria cell images dataset has a simple structure, low noise, and well-defined objects, we decided to apply this approach to it, as you can see in Figure 3.

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4) Gray scale image:

A grayscale image is a form of digital image consisting of shades of grey ranging from black to white. Each pixel in a grayscale image is represented by a single value according to the intensity of light or darkness at that region. Typically, the range of pixel values is between 0 (black) and 255 (white), with values in between indicating shades of grey. This technique is particularly beneficial in instances where the color of a picture is unimportant, or where color may create unnecessary complexity or noise, which is a perfect fit for our segmented, multicoloured image.

One key advantage of this grayscale image is that they require less storage space than full-color images, since each pixel only requires a single value rather than three values for red, green, and blue. This makes them easier to work with in situations where storage capacity is limited or where image processing must be done in real-time.

5) Data augmentation using Generative Adversarial Network (GAN):

Generative Adversarial Networks, often known as GANs, are a specific method of deep learning that can be applied to the process of data augmentation. GANs are made up of two neural networks that collaborate with one another and perform the functions of a generator and a discriminator. The generator network receives input in the form of random noise and produces synthetic data that is designed to be like the data that was originally collected. On the other hand, the discriminator network tries to differentiate between the raw data that was initially collected and the synthetic data that was produced by the generator [11].

During training, the generator network aims to provide synthetic data that is convincing to the discriminator network because of its high degree of similarity to the original data. In the meantime, a discriminator network is being trained to spot discrepancies between the real data and the generated data. The generator network improves over time to the point where its synthetic data can be indistinguishable from the real thing.

In cases where there is insufficient data for training, data augmentation with GANs can be especially helpful. GANs can effectively increase the amount of the dataset and enhance the performance of machine learning models by producing synthetic data that closely mimics the original data. To further address overfitting concerns, GANs can be utilized to produce data which is more diverse than the original dataset. For training deep learning models with little data, such as our malaria dataset, GAN is a robust method of data augmentation that can be utilized to improve model performance.

C. Classification Stage:

Classification models that have shown tremendous promise in the accurate classification of malaria-infected and uninfected cells in medical imaging have been explored. Convolutional Neural Networks (CNN), Residual Neural Networks (ResNet50), and Visual Geometry Group (VGG19) are implemented on the malarial dataset for proper classification. Convolutional layers, pooling layers, and fully linked layers work together in these models to identify important characteristics in images and assign them to the appropriate categories.

Using the Adam optimizer and these classification models, a proper distinguish between infected and uninfected cells in malaria parasites with a high degree of certainty is achieved. An extensively used optimization method, the Adam optimizer updates weights to decrease the loss function. One way to shorten the duration required to train a deep learning model is via the Adam optimizer. The name Adam comes from the concept of adaptive moment estimate. Unlike stochastic gradient descent, which uses a constant learning rate during training, this method varies the learning rate for each weight in the network independently (SGD). A mini-batch gradient descent takes a non-linear path to learning or convergence. Thus, zigzagging takes a considerable amount of time. Adam Optimizer makes the zigzag path more linear by boosting horizontal movement and lowering vertical movement. Training sophisticated and huge models like CNN, ResNet50, and VGG19 is a breeze with its efficient gradient descent and customizable learning rate. In locations where resources and medical experience may be few, such models may help doctors make a quick and accurate diagnosis of malaria. So, the optimization methods may be selected correctly based on the requirements and the type of data used, and Adam performs admirably on this thick blood smear images dataset.

1) Convolutional Neural Network (CNN):

From Figure 4, we can define that a convolutional neural network (CNN) is a type of artificial neural network which has a sequential design of series of convolution and max pooling layers before a fully connected layer to process and analyze data that has a grid-like structure, such as images, videos, and audio signals. The primary goal of CNN is to extract relevant features from the input data using convolutional filters, and then use those features to make accurate predictions.

The convolutional layer is the most important part of CNN. To generate feature maps, this layer applies a series of filtration to the input data and slides them across the full data set. A filter is a tiny, weighted matrix that is trained to recognize a particular kind of feature, such as an edge, texture, or form, in the input data. To provide non-linearity to the model and aid in the capture of more complex patterns, the result of the convolutional layer is routed through a non-linear activation function such as the rectified linear unit (ReLU).

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One or more pooling layers follow the convolutional layers to minimize the dimension of the feature maps and improve CNN's performance. The max pooling technique is widely used because it takes the maximum value from each local area of the feature map. The last layers of a convolutional neural network (CNN) are generally fully connected layers that translate the flattened output of the preceding layers to the expected outcome, such as a classification label. Regularization strategies, such as dropout, may be used in the fully linked layers as well to avoid overfitting.

Training a CNN entails minimizing a loss function, such as cross-entropy, which quantifies the dissimilarity between the anticipated and actual outputs by adjusting the weights of both the filters and fully connected layers. Backpropagation is used for this purpose; it is a method that adjusts the weights in the inverse direction of the gradient of the loss with respect to each weight. Overall, CNN has transformed numerous industries, including computer vision, natural language processing, and robotics, that rely on processing visual input. Object identification, face detection, and image segmentation are just a few of the many fields that have benefited from their capacity to extract useful characteristics from raw data.

An overview of the pseudo code of a Convolutional Neural Network (CNN) for binary classification problem is as follows:

1. Set the network's default values (weights and biases)
2. prepare the data ahead of time (e.g., normalization, resize, etc.)
3. Loop for each layer in the network:
    a. Convolve the input data with the layer's weights.
    b. Use an activation function, such as ReLU, on the output.
    c. Perform pooling operation (e.g., max pooling)
4. Flatten the layer's output.
5. Send the flattened output to an interconnected layer (also known as a dense layer)
6. Use an activation function on the dense layer's output
7. Steps 5 and 6 should be repeated until the necessary number of dense layers has been attained.
8. For binary prediction, use a final dense layer with a single neuron and a sigmoid activation function.
9. Calculate the loss (binary cross-entropy, for example) between the estimated output and the correct output.
10. Employ an optimization method to backpropagate the error and adjust the network's parameters (e.g., stochastic gradient descent, Adam, etc.)
11. Repeat from Step 3 until the appropriate number of epochs has passed. 12. Generate predictions using the trained network on untrained or test data.

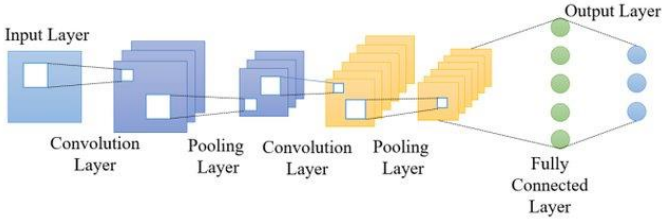

Figure 4: Architecture of Convolutional Neural Network (CNN) [22].

2) Residual Network 50 (ResNet50):

In 2016, researchers Kaiming He, Xiangyu Zhang, Shaoqing Ren, and Jian Sun from Microsoft Research Asia published a paper titled "Deep Residual Learning for Image Recognition," in which they presented the ResNet50 CNN architecture. The purpose of this research was to find a way to prevent the reliability of deep neural networks from decreasing with increasing network depth.

The researchers observe that the vanishing gradient issue makes it such that a neural network's depth is not necessarily proportional to its performance improvement. The training process stalls, and accuracy drops when gradient signals are too weak to go across the network. The authors suggest the ResNet50 design to solve this issue by introducing a skip link, or short cut, that allows gradient signals to skip across one or more network layers.

Figure 5 shows that the ResNet50 architecture has 50 layers where 49 of which are convolutional and 1 of which is fully linked. Residual blocks are the fundamental unit of the design; these blocks include fast-track connections that skip through one or more convolutional layers. Each residual block is comprised of two or three convolutional layers, a batch normalization layer, and an activation function based on the ReLU activation function. Before being fed into the activation function, the output of the second convolutional layer receives the skip connection and is combined with the output of the last layer in the block. Using the ImageNet dataset—1.2 million training images and 50,000 validation images over 1,000 classes—the ResNet50 architecture beats the state-of-the-art deep neural networks. An error rate of 3.57% was attained, which is far lower than the error rates of the old record models.

Since its development, ResNet50 has gained widespread acceptance as a go-to architecture for several computer vision workloads. Because of its superiority in overcoming vanishing gradients, several different residual designs have been developed; yet it continues to serve as a benchmark for deep neural networks.

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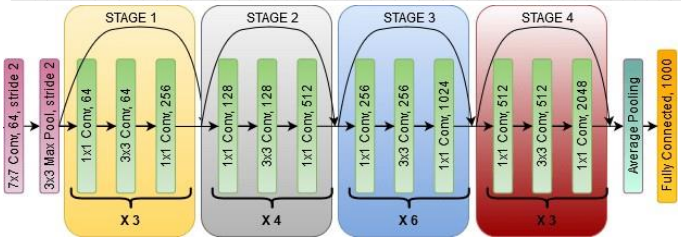

Figure 5: Architecture of Residual Neural Network (ResNet50) [23].

An illustration of the pseudo code for ResNet50, a deep residual network design, for binary classification problem is as follows:

1. Set the network's initial values (weights and biases)
2. Pre-process the input data (e.g., normalization, resize, etc.)
3. Implement the residual block:
    a. Using the block's weights to do a convolution operation on the input data.
    b. Apply batch normalization to the result.
    c. Apply an activation function (such as ReLU) to the result.
    d. Repeat the convolution with the block's weights.
    e. Apply batch normalization to the result.
    f. Add the input data to the result of step e.
4. If more residual blocks are needed, return to Step 3.
5. To minimize the output's spatial dimensions, use a global average pooling technique.
6. Use a single sigmoid-activated neuron in a final dense layer to make a binary prediction.
7. Calculate the loss (binary cross-entropy, for example) between the actual output and the predicted output.
8. Using an optimization technique, backpropagate the error and improve the network's values (e.g., Adam)
9. Repeat Step 3 until you reach the number of epochs you desire.
10. Generate predictions using the trained network on untrained or test data.

3) VGG19 (Frozen CNN):

In the study of "Very Deep Convolutional Networks for Large-Scale Image Recognition," published in 2014, Karen Simonyan and Andrew Zisserman of Oxford University presented the VGG19 deep convolutional neural network (CNN) architecture. State-of-the-art performance was obtained on the ImageNet dataset, which was the intended application of the design, which was to create a broader and more efficient neural network for image classification tasks. Figure 6 shows that the VGG19 architecture has 19 layers total, including 16 convolutional layers, 3 fully linked layers, and an output layer with a SoftMax activation function. Tiny 3x3 filters are used in the convolutional layers, whereas 2x2 filters with stride 2 are used in the pooling layers. In addition to preventing overfitting, the smaller filter size also enables the network to collect more fine-grained data.

The "Xavier initialization" weight initialization approach is one of the major contributions of the VGG19 architecture. The number of input connections to each neuron is denoted by n, and the weights of the convolutional layers are first seeded with a Gaussian distribution with mean 0 and variance 2/n. This starting strategy protects against the vanishing gradient issue and accelerates training by allowing for quicker convergence.

With a top-5 error rate of 7.3% on the ImageNet dataset, the VGG19 architecture showed exceptional accuracy. The authors also demonstrated that the architecture was robust to transfer learning and could be successfully applied to additional computer vision tasks, such as object identification and semantic segmentation. The VGG19 design has been used as a standard measure of deep neural network effectiveness since its development. Its tiny filters and Xavier initialization approach have made it a popular architecture for many computer vision applications, and its simple yet effective design has made it widely used. Here you'll see a pseudocode for VGG19 that's quite like CNNs, since the two employ the same neural network layers while having different architectures. Smaller convolutional filters, many stacked layers, and max pooling for down-sampling are what set VGG19 apart. It was also pretrained on massive amounts of images data.

An overview of the pseudo code of a Visual Geometry Group (VGG19) for binary classification problem is as follows:

1. Set the network's default values (weights and biases)
2. prepare the data ahead of time (e.g., normalization, resize, etc.)
3. Loop for each layer in the network:
    a. Convolve the input data with the layer's weights.
    b. Use an activation function, such as ReLU, on the output.
    c. Perform pooling operation (e.g., max pooling)
4. Flatten the layer's output.
5. Send the flattened output to an interconnected layer (also known as a dense layer)
6. Use an activation function on the dense layer's output.
7. Steps 5 and 6 should be repeated until the necessary number of dense layers has been attained.
8. For binary prediction, use a final dense layer with a single neuron and a sigmoid activation function.
9. Calculate the loss (binary cross-entropy, for example) between the estimated output and the correct output.
10. Employ an optimization method to backpropagate the error and adjust the network's parameters (e.g., stochastic gradient descent, Adam, etc.)
11. Repeat from Step 3 until the appropriate number of epochs has passed.

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12. Generate predictions using the trained network on untrained or test data.

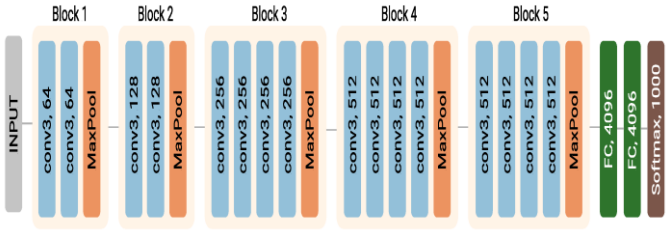

Figure 6: Architecture of Visual Geometry Group (VGG19) Neural Network [24].

D. Evaluation Metrics:

Metrics for measuring the effectiveness of models are crucial in deep learning. The metrics utilized are accuracy, loss, precision, recall and F1 score. These metrics allow for direct comparisons across models, facilitating the selection of the most suitable model for a given application. Brief descriptions of some of the metrics utilized in this research are as follows:

1) Accuracy:

In the context of deep learning, accuracy is a standard measure of performance. It's the proportion of successful predictions to total model predictions.

Accuracy = (number of correct predictions) / (total number of predictions)

2) Loss:

It is the ratio of the actual values to the anticipated values. In modelling, decreasing the loss function is the primary objective.

Loss = (1/ Total number of samples) * ∑ (actual - predicted) ^2

3) Precision:

It is the ratio of the number of positive outcomes (true positives) that were accurately anticipated to the total number of positive outcomes that were predicted.

Precision = (true positives) / (true positives + false positives)

4) Recall:

It is the ratio of the number of true positives to the total number of actual positives.

Recall = (true positives) / (true positives + false negatives)

5) F1 Score:

It is the harmonic mean of precision and recall and a better metric than accuracy in cases where there is an imbalance in the classes.

F1 score = 2 * ((precision * recall) / (precision + recall))

Overall, precision indicates how well the model can predict positive instances, recall measures how well the model can identify all positive cases, and F1 score is a combination of precision and recall. Loss quantifies the discrepancy between anticipated and actual values.

IV. Results and Discussion

This section presents the findings of our study and their implications of malaria diagnosis using deep learning approaches associated with image enhancement and augmentation techniques. We describe the statistical analyses conducted on the malaria dataset and summarize the results which are shown in the following subsections using the evaluation metrics mentioned in the last subsection of methodology. Finally, we include some context on discussion of the significance of the findings, as well as any limitations of the study.

The significance of an accuracy curve increases if it is correct throughout training and validation. When there is a discrepancy between the precision of the training data and the validation data, overfitting is clearly apparent. Figures 7, 9, and 11 depict the accuracy plots (on both training and testing data) for three pre-existing deep learning models: CNN, ResNet50, and VGG19 respectively. Meanwhile, figures 8, 10, and 12 showcase the accuracy plots (on both training and testing data) for three proposed deep learning models which are integrated with the MBOT technique utilized in the pre-processing stage. The X-axis displays the number of epochs utilized and the Y-axis shows the model accuracy. The blue and orange lines represent the training and testing accuracy curves, respectively, based on the number of epochs. Upon examining the graphs, it's evident that the proposed method (with MBOT integration) exhibits more similarity between the training and testing accuracy curves compared to the pre-existing models, indicating that the proposed method is more accurate and less prone to overfitting compared to the existing deep learning models. As the gap deepens, so does the overfitting. Accuracy graph of utilized models are as follows:

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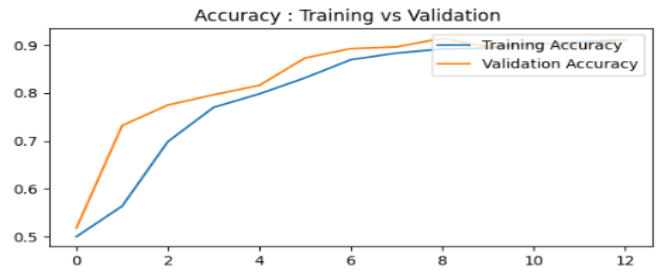

Figure 7: CNN accuracy chart.

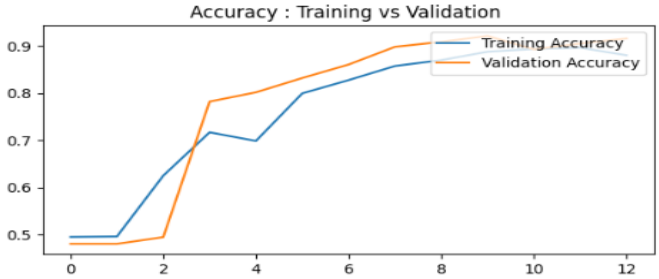

Figure 8: CNN with MBOT accuracy chart.

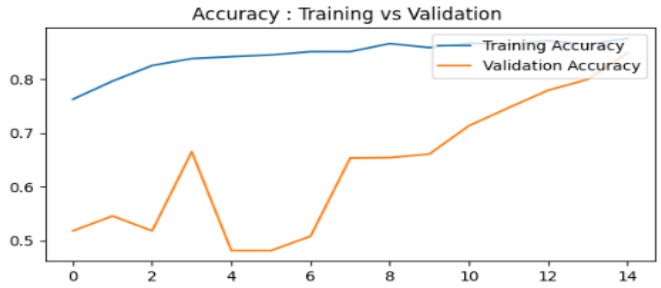

Figure 9: ResNet50 accuracy chart.

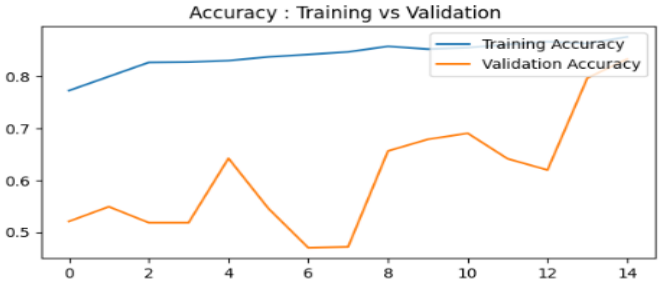

Figure 10: ResNet50 with MBOT accuracy chart.

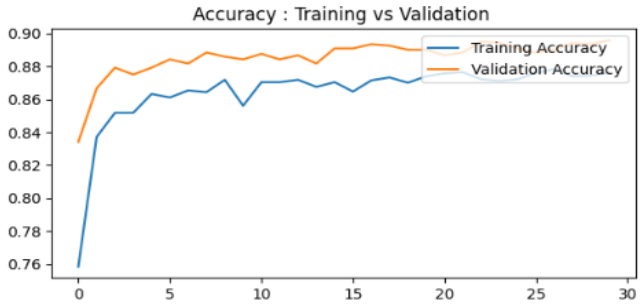

Figure 11: VGG19 accuracy chart.

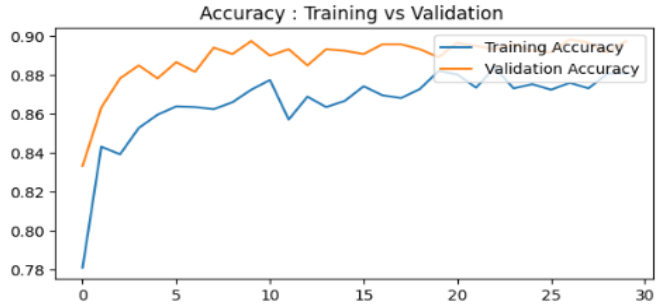

Figure 12: VGG19 with MBOT accuracy chart.

It is guaranteed that the quantitative loss value will be provided at the specified epoch, which is calculated using the loss function over all data items in the epoch. Loss is only seen, however, when the curve is shown over iterations for a subset of the whole dataset. There is much to be learned from a plot of validation loss plus training loss. The loss plots for three prominent deep learning models, which are CNN, ResNet50, and VGG19, are shown in Figures 13, 15, and 17, respectively. Loss plots (on training and testing data) for the three mentioned deep learning models linked with the MBGT approach used in the pre-processing step can be seen in Figures 14, 16, and 18. The model loss is shown on the Y-axis, while the epoch count is shown on the X-axis. Each loss curve for training and testing is shown by a blue and an orange line, respectively, based on the number of iterations or epochs utilized. The figures show that the suggested technique (with MBOT integration) has a closer relationship between the training and testing loss curves than the existing models, suggesting that those models may produce more faulty predictions. To illustrate this, we plotted the following on models that were used:

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Figure 13: CNN loss chart.

Figure 14: CNN with MBOT loss chart.

Figure 15: ResNet50 loss chart.

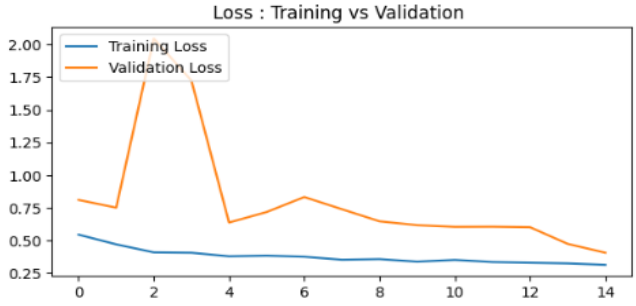

Figure 16: ResNet50 with MBOT loss chart.

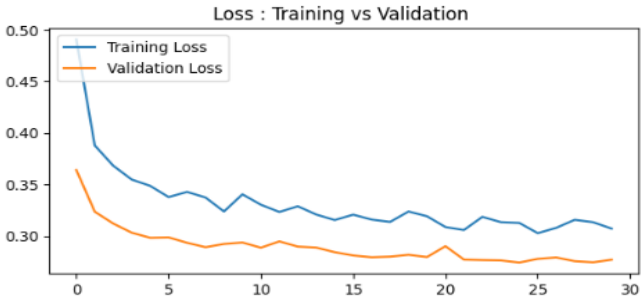

Figure 17: VGG19 loss chart.

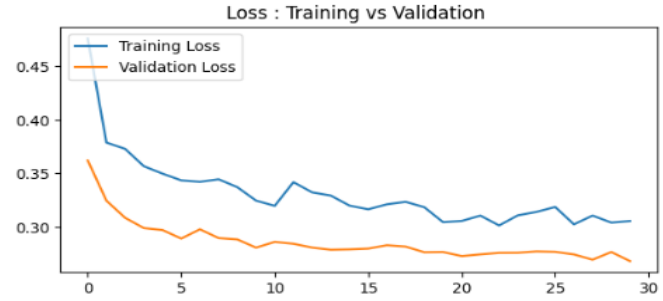

Figure 18: VGG19 with MBOT loss chart.

Table I Comparison of Evaluation metrics of the utilized deep learning models

Parameters / Models	**CNN**	**CNN with MBOT**	**ResNet50**	**ResNet50 with MBOT**	**VGG19**	**VGG19 with MBOT**
Training Accuracy	0.9378	**0.9607**	0.8843	0.9182	0.9542	**0.9846**
Training Loss	0.2312	0.1901	0.4172	0.3652	0.1978	0.1556
Testing Accuracy	0.9157	**0.9508**	0.8783	0.9092	0.9458	**0.9801**
Testing Loss	0.3581	0.2133	0.4256	0.3976	0.2272	0.1680
Precision	0.9300	0.9550	0.8700	0.8950	0.9500	0.9750
Recall	0.9350	0.9550	0.8750	0.8950	0.9450	0.9750
F1-Score	0.9300	0.9500	0.8750	0.8900	0.9550	0.9800

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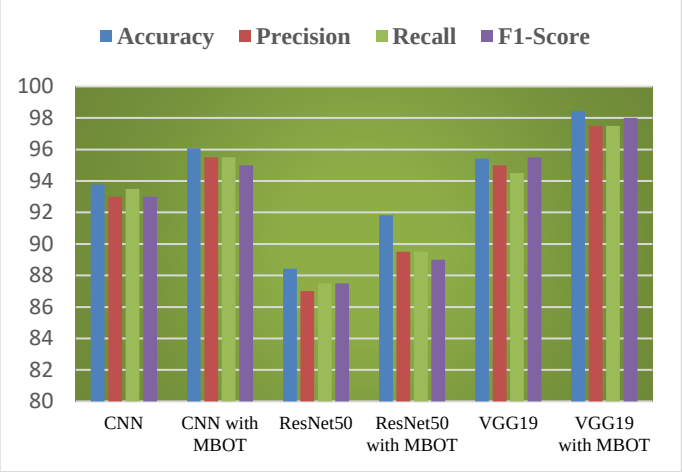

Figure 19: Bar plot of the comparison of training accuracy of the utilized classification models.

Figure 19 shows that the model's performance was enhanced by employing data augmentation, noise reduction, and image segmentation approaches. For this reason, the dropout technique was not implemented. There is a possibility that a faster testing period might benefit the performance of the models as well. Results show that the performance of the suggested neural network model has been greatly improved with the use of this hybrid MBOT approach during the pre-processing step. VGG19 with MBOT outscored CNN and ResNet50 with MBOT in terms of accuracy and loss evaluation criteria, therefore I went with that model. In terms of execution speed, ResNet50 with MBOT is superior to other models.

V. Conclusion

This work presents the enormous potential of deep learning approaches for enhancing the accuracy and speed of malaria diagnosis. For recognizing the Plasmodium parasite in thick blood smear images, the use of deep learning models like VGG19 in combination with noise reduction and image segmentation approaches using GAN as a data augmentation method i.e., VGG19 with MBOT model has shown promising great results by having the accuracy and precision of 98.46% and 97.5% respectively compared to that of other available models such as CNN, ResNet, VGG19, CNN with MBOT and ResNet with MBOT. The VGG19 model might be beneficial in a variety of medical situations due to its mobility and compact design. Furthermore, additional deep learning methods, such as long short-term memory (LSTM) networks and recurrent neural networks (RNNs), may be investigated for use in malaria detection. In addition, the generalizability and robustness of the deep learning models may be improved by using large-scale datasets that incorporate a variety of imaging techniques and combining deep learning algorithms with additional diagnostic tools, including serological testing and PCR, might significantly improve the precision and speed with which malaria is diagnosed.

Conflicts of Interest

The authors declare no conflict of interest.

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